# IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

I hereby certify that this paper is being In the Application of: Loughney deposited with the United States Postal Service in an envelope addressed to the Serial No. To be assigned ) Commissioner for Patents, Washington, ) D.C. 20231 utilizing the "Express Mail Filed: Herewith ) Post Office Addressee" service of the United States Postal Service Under For: Phosphodiesterase 10 Mailing Label No. EK657826395US Group Art Unit: To be assigned Date: February 26, 2002 Examiner: To be assigned Richard Zimmermann

# TRANSMITTAL OF SUBSTITUTE SEQUENCE LISTING

**Assistant Commissioner for Patents** Washington, DC 20231

Sir:

The Applicants respectfully request entry of the substitute Sequence Listing filed herewith. The substitute Sequence Listing corrects errors that were identified during the prosecution of the parent application (USSN 09/256,000) and is included at this time to expedite prosecution.

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted herewith in accordance with 37 C.F.R. §§1.821 and 1.825, are the same, and that the substitute Sequence Listing includes no new matter.

Respectfully submitted,

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Chicago, Illinois 60606-6357

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By

Registration No. 38,659

Attorney for Applicants

### SEQUENCE LISTING

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25

30

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170

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Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val

Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu 105

Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val

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Horas Mans !	Glu			340	Phe				345					350		٠
and the threat	ş	Gln	Gly 355	Met	Ile	Thr	Leu	Ile 360	Leu	Ala	Thr	Asp	Met 365	Ala	Arg	His
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<222> (99)..(443)

<400> 12

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tcc ctg cag agc gac cgt gag aag tca gaa ggc ctt ccc gtg gcc ccg Ser Leu Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro 10 15 20	164
ttc atg gac cga gac aaa gtg acc aag gcc aca gcc cag att ggg ttc Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe 25 30 35	212
atc aag ttt gtc ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc  Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe  40 45 50	260
ccc atg gtt gag gag atc atg ctg cag cca ctt tgg gaa tcc cga gat Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp 55 60 65 70	308
cgc tac gag gag ctg aag cgg ata gat gac gcc atg aaa gag tta cag Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln 75 80 85	356
aag aag act gac agc ttg acg tct ggg gcc acc gag aag tcc aga gag Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu 90 95 100	404
aga agc aga gat gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala 105 110 115	453
ggggggggtg gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg	513
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Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu 35 40 45

Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro 50 55 60

Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp 65 70 75 80

Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala 85 90 95

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Asp Cys Ala 115

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<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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28

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

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90

95

gtc Val 100	cgc Arg	tac Tyr	aat Asn	gac Asp	atc Ile 105	tca Ser	ccg Pro	ctg Leu	Glu	aac Asn 110	cac His	cac His	tgc Cys	gcc Ala	gtg Val 115	451
gcc Ala	ttc Phe	cag Gln	atc Ile	ctc Leu 120	gcc Ala	gag Glu	cct Pro	gag Glu	tgc Cys 125	aac Asn	atc Ile	ttc Phe	tcc Ser	aac Asn 130	atc Ile	499
cca Pro	cct Pro	gat Asp	999 Gly 135	ttc Phe	aag Lys	cag Gln	atc Ile	cga Arg 140	cag Gln	gga Gly	atg Met	atc Ile	aca Thr 145	tta Leu	atc Ile	547
ttg Leu	gcc Ala	act Thr 150	gac Asp	atg Met	gca Ala	aga Arg	cat His 155	gca Ala	gaa Glu	att Ile	atg Met	gat Asp 160	tct Ser	ttc Phe	aaa Lys	595
gag Glu	aaa Lys 165	atg Met	gag Glu	aat Asn	ttt Phe	gac Asp 170	tac Tyr	agc Ser	aac Asn	gag Glu	gag Glu 175	cac His	atg Met	acc Thr	ctg Leu	643
ctg Leu 180	aag Lys	atg Met	att Ile	ttg Leu	ata Ile 185	aaa Lys	tgc Cys	tgt Cys	gat Asp	atc Ile 190	tct Ser	aac Asn	gag Glu	gtc Val	cgt Arg 195	691
cca Pro	atg Met	gaa Glu	gtc Val	gca Ala 200	gag Glu	cct Pro	tgg Trp	gtg Val	gac Asp 205	tgt Cys	tta Leu	tta Leu	gag Glu	gaa Glu 210	tat Tyr	739
ttt Phe	atg Met	cag Gln	agc Ser 215	gac Asp	cgt Arg	gag Glu	aag Lys	tca Ser 220	gaa Glu	ggc Gly	ctt Leu	cct Pro	gtg Val 225	gca Ala	ccg Pro	787
ttc Phe	atg Met	gac Asp 230	cga 'Arg	gac Asp	aaa Lys	gtg Val	acc Thr 235	aag Lys	gcc Ala	aca Thr	gcc Ala	cag Gln 240	att Ile	ggg ggg	ttc Phe	835
atc Ile	aag Lys 245	ttt Phe	gtc Val	ctg Leu	atc Ile	cca Pro 250	atg Met	ttt Phe	gaa Glu	aca Thr	gtg Val 255	acc Thr	aag Lys	ctc Leu	ttc Phe	883
ccc Pro 260	atg Met	gtt Val	gag Glu	gag Glu	atc Ile 265	atg Met	ctg Leu	cag Gln	Pro	ctt Leu 270	tgg Trp	gaa Glu	tcc <sup>·</sup> Ser	cga Arg	gat Asp 275	931
cgc Arg	tac Tyr	gag Glu	gag Glu	ctg Leu 280	aag Lys	cgg Arg	ata Ile	gat Asp	gac Asp 285	gcc Ala	atg Met	aaa Lys	gag Glu	tta Leu 290	cag Gln	979
aag Lys	aag Lys	act Thr	gac Asp 295	agc Ser	ttg Leu	acg Thr	tct Ser	300 Gly ggg	gcc Ala	acc Thr	gag Glu	aag Lys	tcc Ser 305	aga Arg	gag Glu	1027

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Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly Met Ile

135

130

Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile Met Asp 145 150 155 160

Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu Glu His

Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile Ser Asn 180 185 190

Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys Leu Leu 195 200 205

Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly Leu Pro 210 215 220

Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr Ala Gln 225 230 235 240

Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr Val Thr 245 250 255

Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu Trp Glu 260 265 270

Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala Met Lys 275 280 285

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Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp Cys Ala 305 310 315 320

<210> 18

<211> 1887

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(1672)

<400> 18

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tac Tyr	tgc Cys 30	Asn	tcc Ser	agc Ser	gac Asp	atc Ile 35	atg Met	gac Asp	ctg Leu	ttc Phe	Cys 40	Ile	gcc	acc Thr	Gly	205
					acc Thr 50						Thr					253
					acc Thr											301
					gcc Ala											349
					gcg Ala											397
aaa Lys	atc Ile 110	aat Asn	gaa Glu	ctg Leu	aaa Lys	gct Ala 115	gaa Glu	gtt Val	gca Ala	aat Asn	cac His 120	ttg Leu	gct Ala	gtc Val	cta Leu	445
					ttg Leu 130											493
					aag Lys											541
					ccc Pro											589
	Leu				cgc Arg											637
		Glu			gag Glu											685
					gag Glu 210											733

									•					
								-1	9 -					
					Arg				Asn				agg Arg	781
				Сув				Tyr				Phe	cac His	829
			His			tgc Cys					Ser		gtc Val	877
						gag Glu 275								925
						tgc Cys								973
	_		_			gcc Ala				 _	_			1021
						aac Asn	His					Gln		1069
	_	_			_	aac Asn						_		1117
		_				gga Gly 355								1165
						att								1213
						gag Glu								1261
						atc Ile								1309
						tgt Cys								1357
						ggc Gly 435								1405

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ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag  Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu  465  470  475	)1
gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag 154 Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu 480 485 490	19
ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac 159 Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp 495 500 505	∌,7
agc ttg acg tct ggg gcc acc gag aag tcc aga gag aga agc aga gat 164 Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp 510 515 520	15
gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg  Val Lys Asn Ser Glu Gly Asp Cys Ala  525  530	)2
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ctgggcacct ggcaccacaa gaccatgttt tctaagaacc attttgttca ctgataaaaa 181	۱2
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- Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp 50 55 60
- Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro 65 70 75 80
- Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val
- Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu 100 105 110
  - Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val 115 120 125
  - Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp 130 135 140
  - Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn 145 150 155 160
  - Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro 165 170 175
- Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr 180 185 190
- Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro 195 200 205
- Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu 210 215 220
- Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe 225 230 235 240
- Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His 245 250 255
- Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser 260 265 270

Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala 275 280 285

Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln 290 295 300

Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro 305 310 315 320

Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro 325 330 335

Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile 340 345 350

Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His 355 360 365

Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr 370 375 380

Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys 385 390 395 400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp
405 410 415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys
420 425 430

Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr 435 440 445

Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met 450 455 460

Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu 465 470 475 480

Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile 485 490 495

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<210> 20

<211> 1967

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aaa gct gaa gtt gca aat cac ttg gct gtc cta gag aaa cgc gtg gaa Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu

170

165

ttg Leu	gaa Glu	gga Gly	cta Leu 180	aaa Lys	gtg Val	gtg Val	gag Glu	att Ile 185	gag Glu	aaa Lys	tgc Cys	aag Lys	agt Ser 190	gac Asp	att Ile	577
aag Lys	aag Lys	atg Met 195	agg Arg	gag Glu	gag Glu	ctg Leu	gcg Ala 200	gcc Ala	aga Arg	agc Ser	agc Ser	agg Arg 205	acc Thr	aac Asn	tgc Cys	625
ccc Pro	tgt Cys 210	aag Lys	tac Tyr	agt Ser	ttt Phe	ttg Leu 215	gat Asp	aac Asn	cac His	aag Lys	aag Lys 220	ttg Leu	act Thr	cct Pro	cga Arg	673
cgc Arg 225	gat Asp	gtt Val	ccc Pro	act Thr	tac Tyr 230	ccc Pro	aag Lys	tac Tyr	ctg Leu	ctc Leu 235	tct Ser	cca Pro	gag Glu	acc Thr	atc Ile 240	721 .
gag Glu	gcc Ala	ctg Leu	cgg Arg	aag Lys 245	Pro	acc Thr	ttt Phe	gac Asp	gtc Val 250	tgg Trp	ctt Leu	tgg Trp	gag Glu	ccc Pro 255	aat Asn	769
gag Glu	atg Met	ctg Leu	agc Ser 260	tgc Cys	ctg Leu	gag Glu	cac His	atg Met 265	tac Tyr	cac His	gac Asp	ctc Leu	ggg Gly 270	ctg Leu	gtc Val	817
agg Arg	gac Asp	ttc Phe 275	agc Ser	atc Ile	aac Asn	cct Pro	gtc Val 280	acc Thr	ctc Leu	agg Arg	agg Arg	tgg Trp 285	ctg Leu	ttc Phe	tgc Cys	865
gtc Val	cac His 290	gac Asp	aac Asn	tac Tyr	aga Arg	aac Asn 295	aac Asn	ccc Pro	ttc Phe	cac His	aac Asn 300	ttc Phe	cgg Arg	cac His	tgc Cys	913
ttc Phe 305	tgc Cys	gtg Val	gcc Ala	cag Gln	atg Met 310	atg Met	tac Tyr	agc Ser	atg Met	gtc Val 315	tgg Trp	ctc Leu	tgc Cys	agt Ser	ctc Leu 320	961
cag Gln	gag Glu	aag Lys	ttc Phe	tca Ser 325	caa Gln	acg Thr	gat Asp	atc Ile	ctg Leu 330	atc Ile	cta Leu	atg Met	aca Thr	gcg Ala 335	gcc Ala	1009
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gag Glu	aac Asn 370	cac His	cac His	tgc Cys	Ala	gtg Val 375	gcc Ala	ttc Phe	cag Gln	atc Ile	ctc Leu 380	gcc Ala	gag Glu	cct Pro	gag Glu	1153
tgc Cys 385	aac Asn	atc Ile	ttc Phe	tcc Ser	aac Asn 390	atc Ile	cca Pro	cct Pro	gat Asp	395 395	ttc Phe	aag Lys	cag Gln	atc Ile	cga Arg 400	1201

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	-25-
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	Gln Gly Met Il Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala 405 410 415
	gaa att atg gat tot tto aaa gag aaa atg gag aat ttt gac tac agc 1297
	Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser 420 425 430
	aac gag gag cac atg acc ctg ctg aag atg att ttg ata aaa tgc tgt 1345
	Asn Glu Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys 435 440 445
· :	gat atc tct aac gag gtc cgt cca atg gaa gtc gca gag cct tgg gtg 1393
	Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val 450 455 460
	gac tgt tta tta gag gaa tat ttt atg cag agc gac cgt gag aag tca 1441
	Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser 465 470 475 480
	gaa ggc ctt cct gtg gca ccg ttc atg gac cga gac aaa gtg acc aag 1489 Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys
	485 490 495
	gcc aca gcc cag att ggg ttc atc aag ttt gtc ctg atc cca atg ttt 1537
	Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe 500 505 510
	gaa aca gtg acc aag ctc ttc ccc atg gtt gag gag atc atg ctg cag 1585
- · ·	Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln 515 520 525
	cca ctt tgg gaa tcc cga gat cgc tac gag gag ctg aag cgg ata gat 1633 Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp
	530 535 540
	gac gcc atg aaa gag tta cag aag aag act gac agc ttg acg tct ggg 1681
	Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly 545 550 555 560
	gcc acc gag aag tcc aga gag aga agc aga gat gtg aaa aac agt gaa 1729
•	Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu 565 570 575
	gga gac tgt gcc tgaggaaagc ggggggcgtg gctgcagttc tggacgggct 1781 Gly Asp Cys Ala
•	580
	ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc ctgggcacct ggcaccacaa 1841
	gaccatgttt tctaagaacc attttgttca ctgatacaaa aaaaaaaaa ggaattcatg 1901
	atgctgtaca gaattttatt tttaaactgt cttttaaata atatattctt atacggaaaa 1961
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<210> 21

<211> 580

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<400> 21

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Pro Arg Asn Thr Thr Ile Ser Leu Leu Thr Thr Asp Asp Ala Met Val

Ser Ile Asp Pro Thr Met Pro Ala Asn Ser Glu Arg Thr Pro Tyr Lys
50 55 60

Val Arg Pro Val Ala Ile Lys Gln Leu Ser Ala Asp Val Glu Asp Lys
65 70 75 80

Arg Thr Thr Ser Arg Gly Gln Ser Ala Glu Arg Pro Leu Arg Asp Arg 85 90 95

Arg Val Val Gly Leu Glu Gln Pro Arg Arg Glu Gly Ala Phe Glu Ser 100 105 110

Gly Gln Val Glu Pro Arg Pro Arg Glu Pro Gln Gly Cys Tyr Gln Glu 115 120 125

Gly Gln Arg Ile Pro Pro Glu Arg Glu Glu Leu Ile Gln Ser Val Leu 130 135 140

Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu 145 150 155 160

Lys Ala Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu
165 170 175

Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile 180 185 190

Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys 195 200 205

Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg 210 215 220

Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile 225 230 235 240

Glu	Ala	Leu	Arg	Lys 245.	Pro	Thr	Phe	qaA	Val 250	Trp	Leu	Trp.	Glu	255	Asn
Glu	Met	Leu	Ser 260	Сув	Leu	Glu	His	Met 265	Tyr	His	Asp	Leu	Gly 270	Leu	Val
Arg	Asp	Phe 275	Ser	Ile	Asn	Pro	Val 280	Thr	Leu	Arg	Arg	Trp 285	Leu	Phe	Cys
Val	His 290	Asp	Asn	Tyr	Arg	Asn 295	Asn	Pro	Phe	His	Asn 300	Phe	Arg	His	СЛВ
305			Ala		310					315					3,20
			Phe	325					330					335	
			Asp 340					3,45					350		
		355	Thr				360					365			
	370		His	-		375		•			380				
385			Phe		390					395					400
			Ile	405					410					415	
	. •		Asp 420					425					430		
		435	His				440					445			
	450		Asn			455					460				
465			Leu	•	470					475					480
			Pro	485					490					495	
			Gln 500					505				•	510		
		515	Thr				520	•				525			
Pro	Leu 530		Glu	Ser	Arg	Asp 535	Arg	Tyr	Glu	Glu	Leu 540		Arg	Ile	Asp

Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly 555 545 Ala Thr Glu Lys Ser Arg Glu Arg Ser Arg Asp Val Lys Asn Ser Glu 565 Gly Asp Cys Ala 580 <210> 22 <211> 1457 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (164)..(1453) <400> 22 ggctcccggg cgtcccgggc ccggtggcgg cgcggctgtg gttggctgag cgccgcgggc 60 cgcccccgc ccgcccctc cctgctccc ctcccccgcc tcccgcggcg gctggcgtcg 120 ggaaagtaca gtaaaaagtc cgagtgcagc cgccgggcgc agg atg gga tcc ggc Met Gly Ser Gly • 1 tee tee age tae egg eee aag gee ate tae etg gae ate gat gga ege 223 Ser Ser Ser Tyr Arg Pro Lys Ala Ile Tyr Leu Asp Ile Asp Gly Arg 10 att cag aag gta atc ttc agc aag tac tgc aac tcc agc gac atc atg 271 Ile Gln Lys Val Ile Phe Ser Lys Tyr Cys Asn Ser Ser Asp Ile Met 30 319 gac ctg ttc tgc atc gcc acc ggc ctg cct cgg aac acg acc atc tcc Asp Leu Phe Cys Ile Ala Thr Gly Leu Pro Arg Asn Thr Thr Ile Ser 40 ctg ctg acc acc gac gac gcc atg gtc tcc atc gac ccc acc atg ccc 367 Leu Leu Thr Thr Asp Asp Ala Met Val Ser Ile Asp Pro Thr Met Pro geg aat tea gaa ege aet eeg tae aaa gtg aga eet gtg gee ate aag 415 Ala Asn Ser Glu Arg Thr Pro Tyr Lys Val Arg Pro Val Ala Ile Lys 70 . 75 caa ctc tcc gag aga gaa gaa tta atc cag agc gtg ctg gcg cag gtt Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln Val

95

90

85

gca Ala	gag Glu	cag Gln	ttc Phe	tca Ser 105	Arg	gca Ala	ttc Phe	aaa Lys	Ile 110	Asn	gaa Glu	ctg Leu	aaa Lys	gct Ala 115		511
gtt Val	gca Ala	aat Asn	cac His 120	Leu	gct Ala	gtc Val	cta Leu	gag Glu 125	aaa Lys	cgc Arg	gtg Val	gaa Glu	ttg Leu 130	Glu	gga Gly	559
			gtg Val													607
agg Arg	gag Glu 150	gag Glu	ctg Leu	gcg Ala	gcc Ala	aga Arg 155	agc Ser	agc Ser	agg Arg	acc Thr	aac Asn 160	tgc Cys	ccc Pro	tgt Cys	aag Lys	655
			ttg Leu													703
ccc Pro	act Thr	tac Tyr	ccc Pro	aag Lys 185	tac Tyr	ctg Leu	ctc Leu	tct Ser	cca Pro 190	gag Glu	acc Thr	atc Ile	gag Glu	gcc Ala 195	ctg Leu	751
			acc Thr 200											Met		799
			gag Glu													847
			cct Pro												gac Asp	895
			aac Asn													943
-	_	_	atg Met													991
			acg Thr 280													1039
			cat His													1087
		_	gcg Ala	-	_					Ser		Leu				1135

cac His 325	tgc Cys	gcc Ala	gtg Val	gcc Ala	ttc Phe 330	cag Gln	atc Ile	ctc Leu	gcc Ala	gag Glu 335	cct <sup>.</sup> Pro	gag Glu	tgc Cys	aac Asn	atc Ile 340	1183
ttc Phe	tcc Ser	aac Asn	atc Ile	cca Pro 345	cct Pro	gat Asp	Gly ggg	ttc Phe	aag Lys 350	cag Gln	atc Ile	cga Arg	cag Gln	gga Gly 355	atg Met	1231
atc Ile	aca Thr	tta Leu	atc Ile 360	ttg Leu	gcc Ala	act Thr	gac Asp	atg Met 365	gca Ala	aga Arg	cat His	gca Ala	gaa Glu 370	att Ile	atg Met	1279
gat Asp	tct Ser	ttc Phe 375	aaa Lys	gag Glu	aaa Lys	atg Met	gag Glu 380	aat Asn	ttt Phe	gac Asp	tac Tyr	agc Ser 385	aac Asn	gag Glu	gag Glu	1327
cac His	atg Met 390	acc Thr	ctg Leu	ctg Leu	aag Lys	atg Met 395	att Ile	ttg Leu	ata Ile	aaa Lys	tgc Cys 400	tgt Cys	gat Asp	atc Ile	tct Ser	1375
aac Asn 405	gag Glu	gtc Val	cgt Arg	cca Pro	atg Met 410	gaa Glu	gtc Val	gca Ala	gag Glu	cct Pro 415	tgg Trp	gtg Val	gac Asp	tgt Cys	tta Leu 420	1423
	gag Glu									gaga	a					1457
<210	)> 23	3														
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<212	2> PF	2 <b>T</b>														*
<213	> Ho	omo s	apie	ns				•								
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Met 1	Gly	Ser	Gly	Ser 5	Ser	Ser	Tyr	Arg	Pro 10	Lys	Ala	Ile	Tyr	Leu 15	Asp	
Ile	Asp	Gly	Arg 20	Ile	Gln	Lys	Val	Ile 25	Phe	Ser	Lys	Tyr	Сув 30	Asn	Ser	
Ser	Asp	Ile 35	Met	qaA	Leu	Phe	Cys 40	Ile	Ala	Thr	Gly	Leu 45	Pro	Arg	Asn	
Thr	Thr 50	Ile	Ser	Leu	Leu	Thr 55	Thr	Asp	Asp	Ala	Met 60	Val	Ser	Ile	Asp	
Pro 65	Thr	Met	Pro	Ala	Asn 70	Ser	Ğlu	Arg	Thr	Pro 75	Tyr	Lys	Val	Arg	Pro 80	
		_			_	_	Glu	_			_		<b>a</b> 3 .	0	7	

Leu	Ala	Gln	Val 100	Ala	Glu	Gln	Phe	Ser 105	Arg	Ala	Phe	Lys	Ile 110	Asn	Glu
Leu	Lys	Ala 115	Glu	Val	Ala	Asn	His 120	Leu	Ala	Val	Leu	Glu 125	Lys	Arg	Va
Glu	Leu 130	Glu	Gly	Leu	Lys	Val 135	Val	Glu	Ile	Glu	Lys 140	Cys	Lys	Ser	Asp
Ile 145	Lys	Lys	Met	Arg	Glu 150	Glu	Leu	Ala	Ala	Arg 155	Ser	Ser	Arg	Thr	Asr 160
Сув	Pro	Сув	Lys	Tyr 165	Ser	Phe	Leu	Asp	Asn 170		Lys	Lys	Leu	Thr 175	Pro
Arg	Arg	Asp	Val 180	Pro	Thr	Tyr	Pro	Lys 185	Tyr	Leu	Leu	Ser	Pro 190	Glu	Thi
Ile	Glu	Ala 195	Leu	Arg	Lys	Pro	Thr 200	Phe	Asp	Val	Trp	Leu 205	Trp	Glu	Pro
	210				Суѕ	215					220			٠	
225					11e 230					235			•		240
				245					250					255	
			260		Gln			265					270		
		275			Ser		280					285			
	290				Leu	295					300				
305					Glu 310					315					320
				325	аұЭ				330					335	
Glu	Cys	Asn	Ile 340	Phe	Ser	Asn	Ile	Pro 345	Pro	qaA	Gly	Phe	150	Gln	Ile
		355	•	•	Thr		360					365			
	370				Ser	375					380				
Ser 385	Asn	Glu	Glu	His	Met 390	Thr	Leu	Leu	Lys	Met 395	Ile	L u	Ile	Lys	Cya 400

Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp 405 410 415

Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg 420 425 430

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<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: FLAG epitope

<400> 24

Asp Thr Lys Asp Asp Asp Asp Lys
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<210> 25

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 25

tagaccatgg actacaagga cgacgatgac aagatggacg cattcagaag cact

54

<210> 26

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 26.

cgaggagtca acttcttg